SEQUENCE LISTING

<110> Lovejoy, David Chewpoy, R. Bradley Barsyte, Dalia Rotzinger, Susan

<120> TENEURIN C-TERMINAL ASSOCIATED PEPTIDES (TCAP) AND METHODS AND USES THEREOF

THEREOF											
<130>	090931-360630										
	US 10/510,959 2005-08-10										
	PCT/CA03/00622 2003-05-02										
	US 60/376,879 2002-05-02										
	US 60/377,231 2002-05-03										
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tatggcatga	ctctggacga	ggagaaggcg	cgtgtgctgg	agcaggccag	gcagaaggcg	540
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<211> 251

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<213> Artificial Sequence

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<223> Rainbow Trout Ten M3 carboxy termini of Ten M3

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Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser 20 25 30

Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile 35 40 45

Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn 50 55 60

Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly 100 105 110

Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn 115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg 130 135 140

Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala 165 170 175

Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val 180 185 190

Arg Glu Gly Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg
195 200 205

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val 210 215 220

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg 245 250

<210> 4

<211> 252

<212> PRT

<213> Artificial Sequence

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<223> Mouse Ten M1

<400> 4

Met Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe 1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg 20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val 35 40 45 Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala 50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile 65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu 100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg 130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile 145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Met
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Glu Gln Arg Arg 180 185 190

Leu Gln Glu Gly Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys 195 200 205

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe 210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg 245 250

<210> 5

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M2

<400> 5

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe 1 5 10 15

Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile 20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly 35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val 50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn 65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp 85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr
100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe 130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr 145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp 165 170 175

Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln 180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr 210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser 225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg 245 250

<210> 6

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M3

<400> 6

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe 1 5 10 15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala 20 25 30

Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile 35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn 50 55 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly
100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn 115 120 125 Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg 130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala 165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val 180 185 190

Arg Asp Gly Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val 210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg 245 250

<210> 7

<211> 243

<212> PRT

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<220>

<223> Mouse Ten M4

<400> 7

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe 1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser 20 25 30

Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr 50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Ile Ala Ala Ile 70 Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly 90 Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu 100 105 Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val 115 120 Asn Val Thr Val Ser Gln Ile Asn Thr Met Leu Ile Gln Leu Gln Tyr 130 135 Arg Ala Leu Cys Leu Asn Thr Arg Tyr Gly Thr Thr Val Asp Glu Glu 150 Lys Val Arg Val Leu Glu Leu Ala Arg Gln Arg Ala Val Arg Gln Ala 170 165 Trp Ala Arg Glu Gln Gln Arg Leu Arg Glu Gly Glu Gly Leu Arg 180 185 Ala Trp Thr Asp Gly Glu Lys Gln Gln Val Leu Asn Thr Gly Arg Val 195 200 205

Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Met 225 230 235 240

Gln Gly Tyr Asp Gly Phe Phe Val Thr Ser Val Glu Gln Tyr Pro Glu

215

Gly Arg Arg

210

<210> 8

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

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<400> 8

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Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg 20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val 35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala 50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile 65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu 100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg 130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile 145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile 165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg 180 185 190

Leu Gln Glu Gly Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys
195 200 205

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe 210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg 245 250

<210> 9

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Ten M2

<400> 9

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe 1 5 10 15

Met Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile 20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly 35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val 50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn 65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp 85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ser Ala Asp Gly Asp Leu Val Thr 100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val 115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe 130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg T 145 150 155 1	'yr .60								
Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu A	.sp								
Gln Ala Arg Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln G 180 185 190	ln								
Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly G 195 200 205	·lu								
Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly T 210 215 220	yr								
Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser S 225 230 235 2	er 40								
Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg 245 250									
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Gly Gly Ala Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu I 35 40 45	le								

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn 50 55 60

Val 65	Leu	Asn	Ile	Ala	Asn 70	Glu	Asp	Cys	Ile	Lys 75	Val	Ala	Ala	Val	Leu 80
Asn	Asn	Ala	Phe	Tyr 85	Leu	Glu	Asn	Leu	His 90	Phe	Thr	Ile	Glu	Gly 95	Lys
Asp	Thr	His	Tyr 100	Phe	Ile	Lys	Thr	Thr 105	Thr	Pro	Glu	Ser	Asp 110	Leu	Gly
Thr	Leu	Arg 115	Leu	Thr	Ser	Gly	Arg 120	Lys	Ala	Leu	Glu	Asn 125	Gly	Ile	Asn
Val	Thr 130	Val	Ser	Gln	Ser	Thr 135	Thr	Val	Val	Asn	Gly 140	Arg	Thr	Arg	Arg
Phe 145	Ala	Asp	Val	Glu	Met 150	Gln	Phe	Gly	Ala	Leu 155	Ala	Leu	His	Val	Arg 160
Tyr	Gly	Met	Thr	Leu 165	Asp	Glu	Glu	Lys	Ala 170	Arg	Ile	Leu	Glu	Gln 175	Ala
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Arg	Asp	Gly 195	Glu	Glu	Gly	Ala	Arg 200	Leu	Trp	Thr	Glu	Gly 205	Glu	Lys	Arg
Gln	Leu 210	Leu	Ser	Ala	Gly	Lys 215	Val	Gln	Gly	Tyr	Asp 220	Gly	Tyr	Tyr	Val
Leu 225	Ser	Val	Glu	Gln	Tyr 230	Pro	Glu	Leu	Ala	Asp 235	Ser	Ala	Asn	Asn	Ile 240
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Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser 20 25 30

Cys Leu Gln Ala Pro Lys Thr Lys Lys Phe Ala Ser Ser Gly Ser Val 35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr 50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Val Ala Ala Ile 65 70 75 80

Leu Asn His Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu 100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Val Leu Ser Gly Arg Thr Arg 130 135 140

Arg Tyr Thr Asp Ile Gln Leu Gln Tyr Gly Ala Leu Cys Leu Asn Thr 145 150 155 160

Arg Tyr Gly Thr Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Leu 165 170 175

Ala Arg Gln Arg Ala Val Arg Gln Ala Trp Ala Arg Glu Gln Gln Arg 180 185 190

Leu Arg Glu Gly Glu Gly Leu Arg Ala Trp Thr Glu Gly Glu Lys
195 200 205

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe 210 215 220 Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg 245 250

<210> 12

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<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish Ten M3

<400> 12

Ser Ile Ser Gly Val Gln Gln Glu Val Met Arg Gln Ala Lys Ala Phe 1 5 10 15

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser 20 25 30

Ser Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile 35 40 45

Gly Lys Gly Val Met Leu Ala Ile Thr Ser Lys Gly Gln Val Ala Thr 50 55 60

Asn Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Val Thr Val 65 70 75 80

Leu Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu 100 105 110

Gly Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val 115 120 125

Asn Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg 130 135 140 Arg Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val 145 150 155 Arg Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln 165 170 Ala Arg Gln Arg Ala Leu Ser Ser Ala Trp Ala Arg Glu Gln Gln Arg 180 185 Val Arg Asp Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys 195 200 Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr 210 215 Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn 225 Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg 245 <210> 13 <211> 40 <212> PRT <213> Artificial Sequence <220> <223> Rainbow Trout TCAP3 (40a.a.) <400> 13 Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val 5 10 15 Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile 20 25 Gln Phe Leu Arg Gln Ser Glu Ile 35 <210> 14 <211> 41

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<213> Artificial Sequence

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Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
                               25
Ile Gln Phe Leu Arg Gln Ser Glu Ile
       35
<210> 15
<211> 43
<212> PRT
<213> Artificial Sequence
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<223> Rainbow Trout preTCAP3 (43 a.a.)
<400> 15
Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
                5
                                    10
Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20
                                25
Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35
<210> 16
<211> 44
<212> PRT
<213> Artificial Sequence
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<223> Rainbow Trout preTCAP3 (44 a.a.)
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Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20
                                25
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gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa
                                                                    120
                                                                     132
atagggaaga gg
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<223> Zebrafish TCAP3 (40 a.a.)
<400> 21
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               5
                                   10
                                                        15
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
           20
                                25
Gln Phe Leu Arg Gln Ser Glu Ile
        35
<210> 22
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Zebrafish TCAP3 (41 a.a.)
<400> 22
Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
                5
                                    10
                                                        15
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
Val Gln Phe Leu Arg Gln Ser Glu Ile
        35
<210> 23
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<211> 43

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<212> PRT
<213> Artificial Sequence
<223> Zebrafish preTCAP3 (43 a.a.)
<400> 23
Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
                                   10
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
           20
Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35
<210> 24
<211> 44
<212> PRT
<213> Artificial Sequence
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<223> Zebrafish preTCAP3 (44 a.a.)
<400> 24
Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
                                    10
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
            20
                                25
Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
                            40
<210> 25
<211> 120
<212> DNA
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<223> Zebrafish TCAP3 (120 n.a.)
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cagttgctca gctctgggaa ggtgctgggt tacgatggtt actatgtact atcagtggag
                                                                     60
caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata
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<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Zebrafish TCAP3 (123 n.a.)
<400> 26
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gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag
                                                                     120
ata
                                                                     123
<210> 27
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> Zebrafish TCAP3 (129 n.a.)
<400> 27
cagttgctca gctctgggaa ggtgctgggt tacgatggtt actatgtact atcagtggag
                                                                      60
caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata
                                                                     120
                                                                     129
gggaagagg
<210> 28
      132
<211>
<212> DNA
<213> Artificial Sequence
<220>
      Zebrafish preTCAP3 (132 n.a.)
<223>
<400>
      28
aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg
                                                                      60
gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag
                                                                     120
                                                                     132
atagggaaga gg
<210> 29
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Zebrafish TCAP4 (40 a.a.)
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<400> 29

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val 20 25 30

His Phe Trp Arg Gln Thr Glu Met 35 40

<210> 30

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (41 a.a.)

<400> 30

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr 1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn 20 25 30

Val His Phe Trp Arg Gln Thr Glu Met 35 40

<210> 31

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (43 a.a.)

<400> 31

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile 1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val 20 25 30

His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
35 40

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<210> 32
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Zebrafish preTCAP4 (44 a.a.)
<400> 32
Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
                                    10
Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
                                25
           20
Val His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
<210> 33
<211>
      120
<212> DNA
<213> Artificial Sequence
<220>
<223> Zebrafish TCAP4 (120 n.a.)
<400> 33
cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac
                                                                      60
cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg
                                                                     120
<210> 34
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Zebrafish TCAP4 (123 n.a.)
<400> 34
cagcagetee taagetetgg aegtgtacag ggetacgaag gettetacat agtateagte
                                                                      60
gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag
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atg
<210> 35
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<211> 129

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<212> DNA
<213> Artificial Sequence
<220>
<223> Zebrafish preTCAP4 (129 n.a.)
<400> 35
cagetectaa getetggaeg tgtacaggge tacgaagget tetacatagt atcagtegae
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cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg
                                                                     120
                                                                     129
ggacgcagg
<210> 36
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Zebrafish preTCAP4 (132 n.a.)
<400> 36
cagcagetee taagetetgg acgtgtacag ggetacgaag gettetacat agtateagte
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gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag
                                                                     120
                                                                     132
atgggacgca gg
<210> 37
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP1 (40 a.a.)
<400> 37
Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
                                                        15
                                    10
                5
Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
                                                    30
                                25
            20
His Phe Met Arg Gln Ser Glu Ile
        35
<210> 38
<211> 41
<212> PRT
<213> Artificial Sequence
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<220>
<223> Mouse TCAP1 (41 a.a.)
<400> 38
Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
                               25
           20
Ile His Phe Met Arg Gln Ser Glu Ile
<210> 39
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP1 (43 a.a.)
<400> 39
Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20
His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
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<210> 40
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP1 (44 a.a.)
<400> 40
Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
                                25
            20
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Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
                           40
<210> 41
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP1 (120 n.a.)
<400> 41
cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag
                                                                     60
                                                                    120
caqtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata
<210> 42
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP1 (123 n.a.)
<400> 42
cagcagettt tgggcaccgg gagggtgcag gggtatgatg ggtattttgt ettgtetgtt
                                                                     60
gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa
                                                                    120
                                                                    123
ata
<210> 43
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP1 (129 n.a.)
<400> 43
cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag
                                                                     60
cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata
                                                                    120
                                                                    129
ggcaggagg
<210> 44
<211> 132
<212> DNA
<213> Artificial Sequence
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<220>
<223> Mouse preTCAP1 (132 n.a.)
<400> 44
cagcagcttt tgggcaccgg gagggtgcag gggtatgatg ggtattttgt cttgtctgtt
                                                                    60
gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa
                                                                    120
                                                                    132
ataggcagga gg
<210> 45
<211> 40
<212> PRT
<213> Artificial Sequence
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<223> Mouse TCAP2 (40 a.a.)
<400> 45
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
                                   10
Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
                                25
            20
Gln Phe Leu Arg Gln Asn Glu Ile
        35
<210> 46
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP2 (41 a.a.)
<400> 46
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
                                    10
                                                        15
                5
Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
Ile Gln Phe Leu Arg Gln Asn Glu Met
        35
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<210> 47
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP2 (43 a.a)
<400> 47
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
                                   10
Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
           20
                               25
Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
<210> 48
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP2 (44 a.a.)
<400> 48
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
                                25
            20
Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
                            40
<210> 49
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP2 (120 n.a.)
<400> 49
caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa
cagtacccgg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagagg
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60

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<210> 50
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP 2 (123 n.a.)
<400> 50
cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg
                                                                      60
gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag
                                                                     120
                                                                     123
atg
<210> 51
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP2 (129 n.a.)
<400> 51
caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa
                                                                      60
cagtaccegg agetggcaga cagtageage aacatecagt tettaagaca gaatgagatg
                                                                     120
                                                                     129
ggaaagagg
<210> 52
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
      Mouse preTCAP2 (132 n.a.)
<223>
<400> 52
                                                                      60
cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg
                                                                     120
gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag
                                                                     132
atgggaaaga gg
<210>
       53
<211>
       40
<212> PRT
<213> Artificial Sequence
<220>
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<223> Mouse TCAP3 (40 a.a.)
<400> 53
Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
                                    10
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
                                25
Gln Phe Leu Arg Gln Ser Glu Ile
        35
<210> 54
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP3 (41 a..a)
<400> 54
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
                                    10
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
                                25
            20
Ile Gln Phe Leu Arg Gln Ser Glu Ile
        35
<210> 55
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP3 (43 a.a.)
<400> 55
Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
                                    10
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
```

25

20

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Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
        35
<210> 56
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP3 (44 a.a.)
<400> 56
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
                                    10
                5
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
                                                    3.0
                                25
            20
Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
<210> 57
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP3 (120 n.a.)
<400> 57
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag
                                                                      60
                                                                     120
cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc
<210> 58
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse TCAP3 (123 n.a.)
<400> 58
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcggtg
                                                                      60
qaqcaqtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag
                                                                      120
                                                                      123
atc
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<210> 59
<211> 129
<212> DNA
<213> Artificial Sequence
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<223> Mouse preTCAP3 (129 n.a.)
<400> 59
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                                                                    60
cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc
                                                                    120
                                                                    129
ggcaagagg
<210> 60
<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Mouse preTCAP3 (132 n.a.)
<400> 60
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcggtg
                                                                     60
gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag
                                                                    120
                                                                     132
atcggcaaga gg
<210> 61
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP4 (40 a.a.)
<400> 61
Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
                                                        15
                                    10
                5
Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
            20
His Phe Met Arg Gln Ser Glu Met
        35
<210> 62
<211> 41
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<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse TCAP4 (41 a.a.)
<400> 62
Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
            20
                                25
Ile His Phe Met Arg Gln Ser Glu Met
<210> 63
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP4 (43 a.a.)
<400> 63
Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
           20
                               25
His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
       35
<210> 64
<211> 44
<212> PRT
<213> Artificial Sequence
<220>
<223> Mouse preTCAP4 (44 a.a.)
<400> 64
Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
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Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn 20 25 Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg 40 <210> 65 <211> 120 <212> DNA <213> Artificial Sequence <220> <223> Mouse TCAP4 (120 n.a.) <400> 65 caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60 cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120 <210> 66 <211> 123 <212> DNA <213> Artificial Sequence <220> <223> Mouse TCAP4 (123 n.a.) <400> 66 cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60 gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120 123 atg <210> 67 <211> 129 <212> DNA <213> Artificial Sequence <220> <223> Mouse preTCAP4 (129 n.a.) <400> 67 caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60 cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120 129 ggccgaagg <210> 68

<211> 132

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<212> DNA
<213> Artificial Sequence
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<223> Mouse preTCAP4 (132 n.a.)
<400> 68
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                                                                    60
gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag
                                                                    120
atgggccgaa gg
                                                                    132
<210> 69
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> Human TCAP1 (40 a.a.)
<400> 69
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
                               25
His Phe Met Arg Gln Ser Glu Ile
        35
<210> 70
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Human TCAP1 (41 a.a.)
<400> 70
Gln Gln Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
                               25
            20
Ile His Phe Met Arg Gln Ser Glu Ile
        35
                            40
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<210> 71
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP1 (43 a.a.)
<400> 71
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
                               25
            20
His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
<210> 72
<211> 44
<212> PRT
<213> Artificial Sequence
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<223> Human preTCAP1 (44 a.a.)
<400> 72
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
                5
                                    10
Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
                                                    30
            20
                                25
Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
        35
<210> 73
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP1 (120 n.a.)
<400> 73
cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag
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cagtatt	tag aactttctga cagtgccaat	aatattcact	ttatgagaca	gagcgaaata	120
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<220> <223>	Human TCAP1 (123 n.a.)				
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gagcagt	tatt tagaactttc tgacagtgcc	aataatattc	actttatgag	acagagcgaa	120
ata					123
<210> <211> <212> <213>	75 129 DNA Artificial Sequence				
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cagtatt	ttag aactttctga cagtgccaat	aatattcact	ttatgagaca	gagcgaaata	120
ggcagga	agg				129
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<220> <223>	Human preTCAP1 (132 n.a.)				
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gagcagt	tatt tagaactttc tgacagtgcc	aataatattc	actttatgag	acagagcgaa	120
ataggc	agga gg				132
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<220>
<223> Human TCAP2 (40 a.a.)
<400> 77
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
                               25
           20
Gln Phe Leu Arg Gln Asn Glu Met
<210> 78
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP2 (41 a.a.)
<400> 78
Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
            20
Ile Gln Phe Leu Arg Gln Asn Glu Met
        35
<210> 79
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP2 (43 a.a.)
<400> 79
Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
                                    10
Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
                                25
            20
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Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
       35
                           40
<210> 80
<211>
      44
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP2 (44 a.a.)
<400> 80
Gln Gln Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
               5
                                   10
                                                       15
Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Asn
           20
Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
<210> 81
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP2 (120 n.a.)
<400> 81
cagettetga geacegggeg egtgeaaggg taegagggat attaegtget teeegtggag
                                                                     60
caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg
                                                                    120
<210> 82
<211> 123
<212> DNA
<213> Artificial Sequence
<220>
<223> Human TCAP2 (123 n.a.)
<400> 82
cagcagette tgageacegg gegegtgeaa gggtaegagg gatattaegt getteeegtg
                                                                     60
gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag
                                                                    120
                                                                    123
atg
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<220> <223>	Human preTCAP2 (129 n.a.)	
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caataco	ccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg	120
ggaaaga	agg	129
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gagcaat	cacc cagagettge agacagtage ageaacatee agtttttaag acagaatgag	120
atgggaa	aaga gg	132
	85 40 PRT Artificial Sequence	
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<400>	85	
Gln Leu 1	ı Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val 5 10 15	
Leu Sei	r Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile 20 25 30	
Gln Phe	e Leu Arg Gln Ser Glu Ile	

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<210> 86
<211> 41
<212> PRT
<213> Artificial Sequence
<220>
<223> Human TCAP3 (41 a.a.)
<400> 86
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
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Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
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Ile Gln Phe Leu Arg Gln Ser Glu Ile
<210> 87
<211> 43
<212> PRT
<213> Artificial Sequence
<220>
<223> Human preTCAP3 (43 a.a.)
<400> 87
Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
            20
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Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
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<210> 88
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<400> 88
Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
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Val	Leu	Ser	Val 20	Glu	Gln	Tyr	Pro	Glu 25	Leu	Ala	Asp	Ser	Ala 30	Asn	Asn	L	
Ile	Gln	Phe 35	Leu	Arg	Gln	Ser	Glu 40	Ile	Gly	Arg	Arg						
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atc																	123
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cagt	acc	ccg :	agct	ggcc	ga c	agcg	ccaa	c aa	catc	cagt	taa	tgcg	gca	gagc	gaga	atc	120
gaca	anna	aa															129

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<211> 132
<212> DNA
<213> Artificial Sequence
<220>
<223> Human preTCAP3 (132 n.a.)
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gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag
                                                                     120
atcggcagga gg
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<210> 93
<211> 40
<212> PRT
<213> Artificial Sequence
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<223> Human TCAP4 (40 a.a.)
<400> 93
Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
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His Phe Met Arg Gln Ser Glu Met
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<210> 94
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<212> PRT
<213> Artificial Sequence
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<223> Human TCAP4 (41 a.a.)
<400> 94
Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
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Ile His Phe Met Arg Gln Ser Glu Met
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<210> 95
<211> 43
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<223> Human preTCAP4 (43 a..a)
<400> 95
Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
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Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
<210> 96
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<212> PRT
<213> Artificial Sequence
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<223> Human preTCAP4 (44 a.a.)
<400> 96
Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
               5
                                   10
Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
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Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
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<220>
<223> Human TCAP4 (120 n.a.)
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ggccggagg	129
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gagcagtacc cagaactgtc agacagegec aacaacatec aetteatgag acagagegag	120
atgggccgga gg	132
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<211> 41	

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<213> Artificial Sequence
<223> G. gallus TCAP-1
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Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
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Ile His Phe Met Arg Gln Ser Glu Ile
        35
<210> 102
<211> 41
<212> PRT
<213> Artificial Sequence
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<223> Zebrafish TCAP-4
<400> 102
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Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
           20
                                25
Val His Phe Trp Arg Gln Thr Glu Met
        35
<210> 103
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<212> PRT
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<220>
<223> D. melanogaster Ten-m gene product
<400> 103
Glu Leu Val Gln His Gly Asp Val Asp Gly Trp Asn Gly Asp Ile His
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Ser Ile His Lys Tyr Pro Gln Leu Ala Asp Pro Gly Asn Val Ala Phe 20 25 30

Gln Arg Asp Ala Lys 35

<210> 104

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human CRF TCAP like region

<400> 104

Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg

1 10 15

Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His 20 25 30

Ser Asn Arg Lys Leu Met Glu Ile Ile 35 40

<210> 105

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin TCAP-like region

<400> 105

Asp Asn Pro Ser Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr 1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln 20 25 30

Asn Arg Ile Ile Phe Asp Ser Val 35 40

<210> 106

<211> 38

<212> PRT

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<220> <223> Human urocortin 2 TCAP-like region <400> 106 Ile Val Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Gln Ile Leu Leu 10 Glu Gln Ala Arg Ala Arg Ala Arg Glu Gln Ala Thr Thr Asn Ala 25 20 Arg Ile Leu Ala Arg Val 35 <210> 107 <211> 38 <212> PRT <213> Artificial Sequence <220> <223> Human urocortin 3 TCAP=like region <400> 107 Phe Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Leu Leu Phe Asn Ile Ala Lys Ala Lys Asn Leu Arg Ala Gln Ala Ala Ala Asn Ala His Leu Met Ala Gln Ile 35 <210> 108 <211> 46 <212> PRT <213> Artificial Sequence <220> <223> L. migratoria DP <400> 108 Met Gly Met Gly Pro Ser Leu Ser Ile Val Asn Pro Met Asp Val Leu 10

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<223> A. domesticus DP
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Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Met Arg Glu Leu Gln
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Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
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Ser Pro Thr Ile Ser Ile Thr Ala Pro Ile Asp Val Leu Arg Lys Thr
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Trp Glu Gln Glu Arg Ala Arg Lys Gln Met Val Ala Gln Asn Asn Arg
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Glu Phe Leu Asn Ser Leu Asn
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Ala Asn Arg Asn Phe Leu Asn Asp Ile
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Glu Lys Val Ala Gln Asn Asn Arg Asn Phe Leu Asn Arg Val
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<210> 113
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<223> P. Americana
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Ser Asn Arg Lys Met Met Glu Ile Phe
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Asn Arg Ile Ile Phe Asp Ser Val
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10

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Asn Asp Asp Pro Pro Ile Ser Ile Asp Leu Thr Phe His Leu Leu Arg
1 5
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Asn Met Ile Glu Met Ala Arg Asn Glu Asn Gln Arg Glu Gln Ala Gly
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Leu Asn Arg Lys Tyr Leu Asp Glu Val
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<223> M. Musculus UCN2
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Gln Ile Leu Ala His Val
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Arg Leu Leu Ala His Ile 35	
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cccgc	305
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Caacaa	cycc cccacccyy ayaac	23
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<220>
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<222> (1)..(1)
<223> X=I or L
<220>
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<222> (4)..(4)
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<223> Conserved motif between CRF and TCAP - In middle L/V-L/I-X-V/ali
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<220>
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<223> X=E, N, S or P
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<222> (4)..(4)
<223> X=M, L Q, I or V
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Xaa Xaa Xaa Xaa
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<210> 131
<211> 4
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<213> Artificial Sequence
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      /-aliphatic at carboxy terminus
<220>
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<220>
<221> MISC FEATURE
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      (3)..(3)
<223> X=H or basic residues, K, I, R or Q
<220>
<221> MISC FEATURE
<222> (4)..(4)
<223> X=I, L or F
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Lys Glu Arg Arg Pro Tyr Cys Ser Leu Thr Lys Ser Arg Arg Glu Lys
                        10
gaa agg cgc tat aca aat tcg tcc gcg gac aat gag gag tgt agg gtc
                                                                       154
Glu Arg Arg Tyr Thr Asn Ser Ser Ala Asp Asn Glu Glu Cys Arg Val
ccc acg cag aag tcc tat agt tcc agt gaa acc ttg aaa gct ttc gat
                                                                       202
Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala Phe Asp
                                                                       250
cat gat tat tca cgg ctg ctt tat gga aac aga gta aag gat ttg gtc
His Asp Tyr Ser Arg Leu Leu Tyr Gly Asn Arg Val Lys Asp Leu Val
            55
                                60
                                                    65
                                                                       298
cac aga gaa gcc gac gag tat act aga caa gga cag aat ttt acc cta
His Arg Glu Ala Asp Glu Tyr Thr Arg Gln Gly Gln Asn Phe Thr Leu
        70
                                                                       346
agg cag tta gga gtg tgt gaa tcc gca act cga aga gga gtg gca ttc
Arg Gln Leu Gly Val Cys Glu Ser Ala Thr Arg Arg Gly Val Ala Phe
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85 90 tgt gcg gaa atg ggg ctc cct cac aga ggt tac tcc atc agt gca ggg 394 Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile Ser Ala Gly 100 105 110 115 tca gat gcg gat acg gaa aac gaa gca gtg atg tcc cct gag cat gcc 442 Ser Asp Ala Asp Thr Glu Asn Glu Ala Val Met Ser Pro Glu His Ala 120 atg aga ctt tgg ggc agg ggc gtc aaa tcg ggc cgc agt tcc tgc ctg 490 Met Arg Leu Trp Gly Arg Gly Val Lys Ser Gly Arg Ser Ser Cys Leu tca agc cgg tcc aac tcc gcc ctc acc ctg aca gac acg gag cac gag 538 Ser Ser Arg Ser Asn Ser Ala Leu Thr Leu Thr Asp Thr Glu His Glu aac agg teg gae agt gag age gag caa eet tea aac aac eea ggg caa 586 Asn Arg Ser Asp Ser Glu Ser Glu Gln Pro Ser Asn Asn Pro Gly Gln 170 165 175 ccc acc ctg cag cct ttg ccg cca tcc cac aag cag cac ccg gcg cag 634 Pro Thr Leu Gln Pro Leu Pro Pro Ser His Lys Gln His Pro Ala Gln 190 195 180 185 682 cat cac ccg tcc atc act tcc ctc aat aga aac tcc ctg acc aat aga His His Pro Ser Ile Thr Ser Leu Asn Arg Asn Ser Leu Thr Asn Arg 200 205 730 agg aac cag agt ceg gee ceg eeg get get ttg eee gee gag etg caa Arg Asn Gln Ser Pro Ala Pro Pro Ala Ala Leu Pro Ala Glu Leu Gln acc aca ccc gag tcc gtc cag ctg cag gac agc tgg gtc ctt ggc agt 778 Thr Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp Val Leu Gly Ser aat gta cca ctg gaa agc agg cat ttc cta ttc aaa aca ggg aca ggg 826 Asn Val Pro Leu Glu Ser Arg His Phe Leu Phe Lys Thr Gly Thr Gly 250 acq acq cca ctq ttc aqt acq qca acc ccq gga tac aca atg gca tct 874 Thr Thr Pro Leu Phe Ser Thr Ala Thr Pro Gly Tyr Thr Met Ala Ser 260 265 270 ggc tct gtt tat tct ccg cct acc cgg cca ctt cct aga aac acc cta 922 Gly Ser Val Tyr Ser Pro Pro Thr Arg Pro Leu Pro Arg Asn Thr Leu 280 285 tca aga agt gct ttt aaa ttc aag aag tct tca aag tac tgc agc tgg 970 Ser Arg Ser Ala Phe Lys Phe Lys Lys Ser Ser Lys Tyr Cys Ser Trp 295 300 1018 agg tgc acc gca ctg tgt gct gta ggg gtc tca gtg ctc ctg gcc att

Arg Cys Thr Ala Leu Cys Ala Val Gly Val Ser Val Leu Leu Ala Ile

310 315 320 ctc ctc tcc tat ttt ata gca atg cat cta ttt ggc ctc aac tgg cac 1066 Leu Leu Ser Tyr Phe Ile Ala Met His Leu Phe Gly Leu Asn Trp His 325 330 335 tta cag cag acg gaa aat gac aca ttc gag aat gga aaa gtg aat tct 1114 Leu Gln Gln Thr Glu Asn Asp Thr Phe Glu Asn Gly Lys Val Asn Ser 340 345 gac acc gtg cca aca aac act gta tcg tta cct tct ggc gac aat gga 1162 Asp Thr Val Pro Thr Asn Thr Val Ser Leu Pro Ser Gly Asp Asn Gly a L

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			gga Gly 375			_				_			_	1210
			ggc Gly											1258
	_	_	cag Gln			_	_		_		_			1306
			cag Gln											1354
			tcc Ser											1402
_			att Ile 455		_									1450
			cag Gln											1498
			gat Asp											1546
			gag Glu											1594
			ccc Pro											1642
			tgt Cys											1690

535 540 545

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					tgg Trp 570						1786
					cag Gln						1834
		_	_	_	tcg Ser			_	_	 _	1882
-					gga Gly						1930
	_	_		_	cca Pro	 					1978
					gac Asp 650						2026
					act Thr						2074
_					tca Ser						2122
					tgt Cys						2170
					cct Pro						2218
					agc Ser 730						2266
					aag Lys						2314
					tgc Cys						2362

760 765 770

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tgc Cys											2410
ctc Leu											2458
atg Met 805		_	_	_	_	_	_		_		2506
tgt Cys											2554
aca Thr											2602
ctg Leu											2650
aat Asn								_		_	2698
gga Gly 885											2746
tat Tyr											2794
aat Asn							_				2842
act Thr	_							_			2890
gat Asp											2938
ctc Leu 965											2986
tcc Ser											3034

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300	303	93	,,,	995
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			gca ggg tac aag Ala Gly Tyr Lys	
gtt ctt aag att Val Leu Lys Ile	_		ata ccg ttt aac Ile Pro Phe Asn	
atg aag gtc cat Met Lys Val His			ggg aga ctc ttc Gly Arg Leu Phe	_
aag tgg ttt cct Lys Trp Phe Pro			tac acg ttc atc Tyr Thr Phe Ile	
gat aag acg gac Asp Lys Thr Asp	_	-	tac ggc ttg tca Tyr Gly Leu Ser	
gca gtt gtg tcc Ala Val Val Ser			tcg tgc ttg gac Ser Cys Leu Asp	
act ctc tgg gaa Thr Leu Trp Glu			caa ggc tat gag Gln Gly Tyr Glu	
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			aat tac gtc cgg Asn Tyr Val Arg	

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aaa gat ttt aga Lys Asp Phe Arg		-	cac aga tac tac His Arg Tyr Tyr	_
gct acg gac cca Ala Thr Asp Pro		_	gtc tct gat act Val Ser Asp Thr	
			acg gga gcc aaa Thr Gly Ala Lys	_
			acc ggg gaa cag Thr Gly Glu Gln	
			gga ggc aag gct Gly Gly Lys Ala	
gaa gca acg ctc Glu Ala Thr Leu			gca atc gat aag Ala Ile Asp Lys	
			atc aga aag gtt Ile Arg Lys Val	
			tcc aac gac ctc Ser Asn Asp Leu	
			atg cat atc agc Met His Ile Ser	
			atc aac ccc atg Ile Asn Pro Met	
aac tcc atc tac Asn Ser Ile Tyr			gtt tta cag atc Val Leu Gln Ile	
gaa aac cgt cag Glu Asn Arg Gln			cgg ccc atg cac Arg Pro Met His	
cag gtc cct gga Gln Val Pro Gly			aag cac gcg gtt Lys His Ala Val	

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	aca gac ggg ga Thr Asp Gly Gl 1450	_	eu Val Ala Gly	
	gac tgc aag aa Asp Cys Lys As 1465		sn Cys Asp Cys	
	ggc tac gcc aa Gly Tyr Ala Ly 1480		ys Leu Asn Ala	
tcc tcc ctg gcc Ser Ser Leu Ala	gcc tcg cca ga Ala Ser Pro As 1495		eu Tyr Ile Ala	
ctg gga aat atc Leu Gly Asn Ile	agg atc cgg gc Arg Ile Arg Al 1510		ys Asn Lys Pro	
ctg aac tca atg Leu Asn Ser Met	aac ttt tac ga Asn Phe Tyr Gl 1525		er Pro Thr Asp	
	ttt gac atc aa Phe Asp Ile As 1540		is Gln Tyr Thr	
	ggt gac tac ct Gly Asp Tyr Le 1555		ne Ser Tyr Ser	_
	acc gct gta ac Thr Ala Val Th 1570		sn Gly Asn Thr	
cga atc cga agg Arg Ile Arg Arg	gat ccg aat cg Asp Pro Asn Ar 1585		tg cgg gtg gtg al Arg Val Val	
cct gat aac cag Pro Asp Asn Gln			gc acc aac ggg ly Thr Asn Gly	
ctg aaa agc atg Leu Lys Ser Met			ng gtt ttg ttt eu Val Leu Phe	

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gga tgg aca aca Gly Trp Thr Thr	_		gaa ggt cgc ctg Glu Gly Arg Leu	_
aat gtt acc ttc Asn Val Thr Phe			aac ctg cac ggg Asn Leu His Gly	
atg gac aag gct Met Asp Lys Ala			tca tcc agc aga Ser Ser Ser Arg	
gaa gat gtc agc Glu Asp Val Ser			tcc atc gat tcc Ser Ile Asp Ser	
tac acc atg gtc Tyr Thr Met Val			agt tac cag att Ser Tyr Gln Ile	
tat gat ggc tcc Tyr Asp Gly Ser			agt ggt ctg gac Ser Gly Leu Asp	
cac tac cag aca His Tyr Gln Thr			ggc acg gcg aat Gly Thr Ala Asn	
			ggt gag aac ggg Gly Glu Asn Gly	
			caa gcc cag ggc Gln Ala Gln Gly	
			aat ggg cgc aac Asn Gly Arg Asn	
ctc tca gtg gac Leu Ser Val Asp			acg gaa aag atc Thr Glu Lys Ile	
gat gac cac cgg Asp Asp His Arg			gct tac gac acg Ala Tyr Asp Thr	
ggg cac ccg act Gly His Pro Thr			aag cta atg gca Lys Leu Met Ala	

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aac gtc acc tac Asn Val Thr Tyr			gcc agc atc cag Ala Ser Ile Gln	_
ggg acc acg agc Gly Thr Thr Ser			agc cag ggg agg Ser Gln Gly Arg	
gta tct cgg gtc Val Ser Arg Val			tgg agt tac acg Trp Ser Tyr Thr	
ttg gaa aag tcc Leu Glu Lys Ser		_	agc cag cgg cag Ser Gln Arg Gln	
atc ttc gaa tac Ile Phe Glu Tyr			tcc gcc atc acc Ser Ala Ile Thr	
ccc agt gtg gct Pro Ser Val Ala		atg cag acc Met Gln Thr 1920	atc cgg tcc att Ile Arg Ser Ile	
tac tac cgc aac Tyr Tyr Arg Asn		ccc cca gaa Pro Pro Glu 1935	agc aat gcc tct Ser Asn Ala Ser	
atc acc gac tac Ile Thr Asp Tyr			ctg caa aca gct Leu Gln Thr Ala	
			tat aga agg cag Tyr Arg Arg Gln	
			aga gtc agt ttt Arg Val Ser Phe	
tac gac gaa aca Tyr Asp Glu Thr			gta aac ctt cag Val Asn Leu Gln	
gat ggt ttt att Asp Gly Phe Ile	_		caa att ggt ccc Gln Ile Gly Pro	_
att gac aga cag Ile Asp Arg Gln			gat gga atg gta Asp Gly Met Val	
gcg aga ttt gac Ala Arg Phe Asp	-		ttt cga gtg acc Phe Arg Val Thr	

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cag ttt gat gac Gln Phe Asp Asp			cag ttt gga aaa Gln Phe Gly Lys	
			att tcc acg gcc Ile Ser Thr Ala	
			ggg cgc atc aag Gly Arg Ile Lys	
			tac tgg att aca Tyr Trp Ile Thr	
			aga gag att aaa Arg Glu Ile Lys	
ggg cct ttt gcc Gly Pro Phe Ala			tac gag tac gac Tyr Glu Tyr Asp	_
			gaa aag atc atg Glu Lys Ile Met	
			cac ttg ctc aac His Leu Leu Asn	
			tat gac ctg cgc Tyr Asp Leu Arg	
			cgg ctg gat gaa Arg Leu Asp Glu	
ggt ttc ctg cgt Gly Phe Leu Arg		_	ttt gaa tac agc Phe Glu Tyr Ser	
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gtg atc tat cgg Val Ile Tyr Arg			cgt gtt tct agc Arg Val Ser Ser	

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atc acc tco Ile Thr Sen		Tyr Asp		-						6949
gag atc ago Glu Ile Se										6994
ggg aca ccg Gly Thr Pro		-	-							7039
cag acc cag Gln Thr Gli										7084
gtc gac tt Val Asp Phe		Val Ile								7129
ccg ctc acc Pro Leu Th		Ile His	ttt gga Phe Gly		aga Arg					7174
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aac aac cco Asn Asn Pro		Lys Ile								7309
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gct att cc Ala Ile Pro		Pro Val								7399
tcc tat gag Ser Tyr Gli										7444

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				cag Gln 2500										7579
				ggc Gly 2515										7624
				ctc Leu 2530										7669
				aac Asn 2545		_			ctg Leu 2550					7714
				aag Lys 2560	-				ttc Phe 2565					7759
				ctg Leu 2575										7804
				999 Gly 2590					gtg Val 2595					7849
				agg Arg 2605										7894
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	gag Glu			cgc Arg 2635					gcg Ala 2640	cgc Arg	-	_		7984
_				gca Ala 2650			_	_	cgc Arg 2655		_	_	 -	8029
	ggt Gly		_	ctc Leu					gag Glu					8074

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						cag Gln										211
						agg Arg	_	_						_		259
		_		_		aac Asn		_			_	_	_	_		307
						cag Gln										355
	_				_	gac Asp 90				_		-	_			403
	_		_	_	_	agt Ser	_	_	_	_			_	_	_	451
_		_			_	ctg Leu	_		_			_		_		499
-		-	_	_		gaa Glu										547
			_	-		aag Lys										595
	_	_				atc Ile 170					_				_	643
						gag Glu										691
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						ctc Leu										787

215 220 225

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Gln Asn Glu Met 35

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Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala 50 55 60

Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile Leu 65 70 75 80

Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Arg 85 90 95

Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu Val 100 105 110

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His Phe Met Arg Gln Ser Glu Ile 35 40